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=> d full his

     (FILE 'HOME' ENTERED AT 12:58:39 ON 24 FEB 2002)

     FILE 'REGISTRY' ENTERED AT 12:59:26 ON 24 FEB 2002
L*** DEL      0 S RODA/CN
L*** DEL     34 S RODA

     FILE 'HCAPLUS' ENTERED AT 12:59:51 ON 24 FEB 2002
                E RODA/CT
                E RODA CELL DIVISION/CT
L1           90 SEA ABB=ON  PLU=ON  RODA OR RODA PROTEIN OR RODA CELL DIVISION
                PROTEIN
L2          942 SEA ABB=ON  PLU=ON  CORYNEFORM OR CORYNEFORM BACTERIA OR
                (BACTERIA (L) CORYNEFORM)
L3            0 SEA ABB=ON  PLU=ON  L1 (L) L2
L4           17 SEA ABB=ON  PLU=ON  L1 (L) (DNA OR CDNA OR NUCLEOTIDE OR
                POLYNUCLEOTIDE OR NUCLEIC ACID)
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=> d ibib ab 1-17

L4 ANSWER 1 OF 17 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:98372 HCAPLUS
DOCUMENT NUMBER: 134:232542
TITLE: Genome sequence of enterohemorrhagic Escherichia coli O157:H7
AUTHOR(S): Perna, Nicole T.; Plunkett, Guy, III; Burland, Valerie; Mau, Bob; Glasner, Jeremy D.; Rose, Debra J.; Mayhew, George F.; Evans, Peter S.; Gregor, Jason; Kirkpatrick, Heather A.; Posfai, Gyorgy; Hackett, Jeremiah; Klink, Sara; Boutin, Adam; Shao, Ying; Miller, Leslie; Grotbeck, Erik J.; Davis, N. Wayne; Lim, Alex; Dimalanta, Eileen T.; Potamousis, Konstantinos D.; Apodaca, Jennifer; Anantharaman, Thomas S.; Lin, Jieyi; Yen, Glaex; Schwartz, David C.; Welch, Rodney A.; Blattner, Frederick R.
CORPORATE SOURCE: Genome Center of Wisconsin, Department of Animal Health and Biomedical Sciences, Laboratory of Genetics, Department of Chemistry, Department of Biostatistics, and Department of Medical Microbiology and Immunology, University of Wisconsin, Madison, WI, 53706, USA
SOURCE: Nature (London) (2001), 409(6819), 529-533
CODEN: NATUAS; ISSN: 0028-0836
PUBLISHER: Nature Publishing Group
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The bacterium Escherichia coli O157:H7 is a worldwide threat to public health and has been implicated in many outbreaks of hemorrhagic colitis, some of which included fatalities caused by hemolytic uremic syndrome. Close to 75,000 cases of O157:H7 infection are now estd. to occur annually in the United States. The severity of disease, the lack of effective treatment and the potential for large-scale outbreaks from contaminated food supplies have propelled intensive research on the pathogenesis and detection of E. coli O157:H7. The genome of E. coli O157:H7 was sequenced to identify candidate genes responsible for pathogenesis, to develop better methods of strain detection and to advance our understanding of the evolution of E. coli, through comparison with the genome of the non-pathogenic lab. strain E. coli K-12. Lateral gene transfer found to be far more extensive than previously anticipated. In fact, 1387 new genes encoded in strain-specific clusters of diverse sizes were found in O157:H7. These include candidate virulence factors, alternative metabolic capacities, several prophages, and other new functions - all of which could be targets for surveillance.
REFERENCE COUNT: 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 2 OF 17 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:789389 HCAPLUS
DOCUMENT NUMBER: 135:117725
TITLE: Long-term experimental evolution in Escherichia coli. IX. Characterization of insertion sequence-mediated mutations and rearrangements
AUTHOR(S): Schneider, Dominique; Duperchy, Esther; Coursange, Evelyne; Lenski, Richard E.; Blot, Michel
CORPORATE SOURCE: Laboratoire Plasticite et Expression des Genomes Microbiens, Universite Joseph Fourier, Grenoble, 380419, Fr.
SOURCE: Genetics (2000), 156(2), 477-488
CODEN: GENTAE; ISSN: 0016-6731
PUBLISHER: Genetics Society of America
DOCUMENT TYPE: Journal
LANGUAGE: English
AB As part of a long-term evolution expt., two populations of Escherichia coli B adapted to a glucose minimal medium for 10,000 generations. In both populations, multiple IS-assocd. mutations arose that then went to

fixation. We identify the affected genetic loci and characterize the mol. events that produced nine of these mutations. All nine were IS-mediated events, including simple insertions as well as recombination between homologous elements that generated inversions and deletions. Sequencing **DNA** adjacent to the insertions indicates that the affected genes are involved in central metab. (knockouts of pykF and nadR), cell wall synthesis (adjacent to the promoter of pbpA-**rodA**), and ill-defined functions (knockouts of hokB-sokB and yfcU). These genes are candidates for manipulation and competition expts. to det. whether the mutations were beneficial or merely hitchhiked to fixation.

REFERENCE COUNT: 68 THERE ARE 68 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 3 OF 17 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2000:31297 HCAPLUS
DOCUMENT NUMBER: 132:74556
TITLE: Cloning and sequence of a novel cell surface protein from Staphylococcus aureus and its use to screen for antibacterial agents
INVENTOR(S): Hodgson, John Edward; Burnham, Martin Karl Russell
PATENT ASSIGNEE(S): Smithkline Beecham Plc, UK
SOURCE: U.S., 18 pp.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6013482	A	20000111	US 1996-730261	19961015
US 6299880	B1	20011009	US 1999-366575	19990804

PRIORITY APPLN. INFO.: GB 1995-21148 A 19951016
GB 1996-4594 A 19960304
US 1996-730261 A3 19961015

AB The present invention relates to a novel cell surface protein from S. aureus WCUH29, **DNA** (RNA) encoding such protein and a procedure for producing such proteins by recombinant techniques. The amino acid sequence of novel cell surface protein displays homol. to bacterial **rodA** (LPXTG motif). Also disclosed are methods for utilizing such novel cell surface protein to screen for antibacterial compds. Also disclosed are diagnostic assays for detecting diseases related to the presence of novel cell surface protein **nucleic acid** sequences and the polypeptides in a host. The cell surface protein of the invention may also be used as a vaccine to induce immunol. responses to protect against disease.

REFERENCE COUNT: 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 4 OF 17 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1998:695455 HCAPLUS
DOCUMENT NUMBER: 130:92667
TITLE: Evolutionary relationships in Aspergillus section Fumigati inferred from partial .beta.-tubulin and hydrophobin DNA sequences
AUTHOR(S): Geiser, David M.; Frisvad, Jens C.; Taylor, John W.
CORPORATE SOURCE: Department of Plant and Microbial Biology, University of California, Berkeley, CA, 94720, USA
SOURCE: Mycologia (1998), 90(5), 831-845
CODEN: MYCOAE; ISSN: 0027-5514
PUBLISHER: New York Botanical Garden
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Members of Aspergillus section Fumigati are important animal pathogens and food contaminants. There is considerable variation among the 16 currently recognized species in this section, particularly in their mating systems: five are known to be strictly mitosporic, nine are homothallic, and two

are heterothallic. Phylogenetic relationships were inferred among members of Aspergillus section Fumigati based on partial **DNA** sequences from the benA .beta.-tubulin and **rodA** hydrophobin genes. Aspergillus clavatus was chosen as an outgroup. The two gene regions provided nearly equal nos. of phylogenetically informative **nucleotide** characters. The **rodA** region possessed a considerably higher level of inferred amino acid variation than did the benA region. The results of a partition homogeneity test showed that the benA and **rodA** data sets were not in significant conflict, and the topologies of the most parsimonious trees for the two data sets differed only in branches that were not strongly supported by boot-strapping. The data sets in combination showed that morphol. and secondary metabolite characters used in taxonomy were not strongly correlated with phylogeny. Mixed interrelationships were found among strictly mitotic, homothallic (selfing and outcrossing) and heterothallic (obligately outcrossing) taxa, suggesting multiple independent losses of the Neosartorya sexual state and possible derivation of heterothallism from homothallism through loss of self compatibility. The food spoiling species N. fischeri was identified as the closest known meiotic relative to the cosmopolitan species most often implicated in human aspergillosis, A. fumigatus.

REFERENCE COUNT: 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 5 OF 17 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1996:760035 HCAPLUS

DOCUMENT NUMBER: 126:55663

TITLE: Gene arrangement and organization in a .apprx.76 kb fragment encompassing the oriC region of the chromosome of Mycobacterium leprae

AUTHOR(S): Fsihi, Hafida; De Rossi, Edda; Salazar, Leiria; Cantoni, Rita; Labo, Monica; Riccardi, giovanna; Takiff, Howard E.; Eiglmeier, Karin; Bergh, Staffan; Cole, Stewart T.

CORPORATE SOURCE: Unite Genet. Mol. Bacterienne, Inst. Pasteur, Paris, 75724, Fr.

SOURCE: Microbiology (Reading, U. K.) (1996), 142(11), 3147-3161
CODEN: MROBEO; ISSN: 1350-0872

PUBLISHER: Society for General Microbiology

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A continuous 75627 bp segment of the Mycobacterium leprae chromosome spanning the oriC region was sequenced. The gene order at this locus was similar to that found in the replication origin region of many other prokaryotes, particularly Mycobacterium tuberculosis and Streptomyces coelicolor. As in the case of several Gram-pos. bacteria, essential genes involved in basic cellular functions, such as **DNA** or RNA metab. (dnaA, dnaB, dnaN, gyrB, gyrA, pcnB, recF, rnpA, ssb), cell wall synthesis (ponA, pbpA) and probably cell division (gidB, **rodA**) were found. Strikingly, the gidA gene was absent from this part of the genome and there was no rRNA operon near oriC. The gyrA gene harbors an intein coding sequence indicating that protein splicing is required to produce the mature A subunit of **DNA** gyrase. Among the many other noteworthy features were ORFs encoding putative serine/threonine protein kinases and a protein phosphatase, three tRNA genes, one M. leprae-specific repetitive element and a glnQ pseudogene.

L4 ANSWER 6 OF 17 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1995:522334 HCAPLUS

DOCUMENT NUMBER: 123:29149

TITLE: dewA encodes a fungal hydrophobin component of the Aspergillus spore wall

AUTHOR(S): Stringer, Mary A.; Timberlake, William E.

CORPORATE SOURCE: Department Genetics, University Georgia, Athens, GA, 30602, USA

SOURCE: Mol. Microbiol. (1995), 16(1), 33-44

CODEN: MOMIEE; ISSN: 0950-382X
DOCUMENT TYPE: Journal
LANGUAGE: English
AB An anonymous **cDNA** clone, pCAN4, was shown previously to correspond to an mRNA that accumulates preferentially during asexual sporulation fo the filamentous fungus Aspergillus nidulans. The peptide encoded by pCAN4 is a fungal hydrophobin, a group of small, hydrophobic cell wall proteins. When the CAN4 gene was disrupted, conidia and conidiophores appeared to be normal, but sporulating colonies wetted more rapidly with detergent solns. than did the wild type. We renamed CAN4 dewA for the detergent wettable phenotype and mapped it to chromosome V, 24 map units from cysC. The A. nidulans **rodA** gene also encodes a sporulation-specific fungal hydrophobin. Spores of a dewA- **rodA** - double mutant were less hydrophobic than those of either mutant alone, showing that dewA and **rodA** contribute independently to spore-wall hydrophobicity. Immunolocalization of DewA by epitope tagging demonstrated that DewA is present in the spore wall, but not in the walls of germ tubes, hyphae or cells of the spore-producing conidiophore. We conclude that dewA encodes a new fungal hydrophobin component of the conidial wall.

L4 ANSWER 7 OF 17 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1995:93961 HCAPLUS
DOCUMENT NUMBER: 123:26632
TITLE: Rodletless mutants of Aspergillus fumigatus
AUTHOR(S): Thau, Nathalie; Monod, Michel; Crestani, Bruno; Rolland, Corine; Tronchin, Guy; Latge, Jean-Paul; Paris, Sophie
CORPORATE SOURCE: Unite Mycologie, Institut Pasteur, Paris, F-75724, Fr.
SOURCE: Infect. Immun. (1994), 62(10), 4380-8
CODEN: INFIBR; ISSN: 0019-9567
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Conidia of Aspergillus fumigatus adhere in vitro to host proteins and cells via the outer cell wall layer. The rodA gene of A. fumigatus was cloned by homol. with the rodA gene of Aspergillus nidulans, which is involved in the structure of the rodlets characteristic of the surface layer. The A. fumigatus RODA protein sequence has 85% similarity to that of A. nidulans RODA; the sequence codes for a hydrophobin, a low-mol.-wt. protein moderately hydrophobic and rich in cysteines. The gene was disrupted with the hygromycin B resistance gene. By transformation of protoplasts with the disrupted gene, RodA- mutants were generated. These mutants are deficient in the ability to disperse their conidia; their conidia lack the rodlet layer and are hydrophilic. The adhesion of the rodletless conidia to collagen and bovine serum albumin was lower than that of the wild type; in contrast, there was no difference between RodA- and RodA+ conidia in adhesion to pneumocytes, fibrinogen, and laminin, suggesting that RODA is not the receptor for these cells and proteins. RodA- conidia were pathogenic for mice.

L4 ANSWER 8 OF 17 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1994:647438 HCAPLUS
DOCUMENT NUMBER: 121:247438
TITLE: Bidirectional gene transfer between Aspergillus fumigatus and Aspergillus nidulans
AUTHOR(S): Borgia, Peter T.; Dodge, Carol L.; Eagleton, Lanie E.; Adams, Thomas H.
CORPORATE SOURCE: Department of Medical Microbiology and Immunology and, Springfield, IL, 62794-9230, USA
SOURCE: FEMS Microbiol. Lett. (1994), 122(3), 227-32
CODEN: FMLED7; ISSN: 0378-1097
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A genomic **DNA** library was constructed from a pathogenic strain of Aspergillus fumigatus using the cosmid vector pCosAX. Cosmid clones with homologies to the **rodA**, brlA, fluG, flbA or trpC genes from A. nidulans were isolated from the library. Each A. fumigatus clone was

used to complement a strain of A. nidulans with a mutation in the homologous gene. A spontaneous white spored strain of A. fumigatus was isolated. The mutation was complemented by transforming the strain with a plasmid contg. the wA gene from A. nidulans. The results from these expts. indicate a significant degree of structural and functional homol. between genes from the organisms. These findings indicate the potential to exploit the methods and information available from A. nidulans to address questions related to human disease caused by A. fumigatus and the ability to use A. nidulans as a surrogate genetic host for characterizing A. fumigatus gene function.

L4 ANSWER 9 OF 17 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1994:27250 HCAPLUS
DOCUMENT NUMBER: 120:27250
TITLE: Penicillin-binding protein 2 inactivation in Escherichia coli results in cell division inhibition, which is relieved by FtsZ overexpression
AUTHOR(S): Vinella, Daniel; Joseleau-Petit, Daniele; Thevenet, Danielle; Bouloc, Philippe; D'ari, Richard
CORPORATE SOURCE: Inst. Jacques Monod, Univ. Paris 7, Paris, 75251, Fr.
SOURCE: J. Bacteriol. (1993), 175(20), 6704-10
CODEN: JOBAAY; ISSN: 0021-9193
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Aminoacyl-tRNA synthetase mutants of Escherichia coli are resistant to amdinocillin (mecillinam), a .beta.-lactam antibiotic which specifically binds penicillin-binding protein 2 (PBP2) and prevents cell wall elongation with concomitant cell death. The leuS(Ts) strain, in which leucyl-tRNA synthetase is temp. sensitive, was resistant to amdinocillin at 37.degree.C because of an increased GDP 3'-diphosphate (ppGpp) pool resulting from partial induction of the stringent response, but it was sensitive to amdinocillin at 25.degree.C. A leuS(Ts) .DELTA. (**rodA**-pbpA)::Kmr strain, in which the PBP2 structural gene is deleted, was constructed. This strain grew as spherical cells at 37.degree.C but was not viable at 25.degree.C. After a shift from 37 to 25.degree.C, the ppGpp pool decreased and cell division was inhibited; the cells slowly carried out a single division, increased considerably in vol., and gradually lost viability. The cell division inhibition was reversible when the ppGpp pool increased at high temp., but reversion required de novo protein synthesis, possibly of septation proteins. The multicopy plasmid pZAQ, overproducing the septation proteins FstsZ, FtsA, and FtsQ, conferred amdinocillin resistance on a wild-type strain and suppressed the cell division inhibition in the leuS(Ts) .DELTA.(rod4-pbpA)::Kmr strain at 25.degree.C. The plasmid pAQ, in which the ftsZ gene is inactivated, did not confer amdinocillin resistance. It is hypothesized that the **nucleotide** ppGpp activates ftsZ expression and thus couples cell division to protein synthesis.

L4 ANSWER 10 OF 17 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1994:4141 HCAPLUS
DOCUMENT NUMBER: 120:4141
TITLE: Penicillin-binding proteins from Erwinia amylovora: mutants lacking PBP2 are avirulent
AUTHOR(S): Milner, J. S.; Dymock, D.; Copper, R. M.; Roberts, I. S.
CORPORATE SOURCE: Dep. Microbiol., Univ. Leicester, Leicester, LE1 9HN, UK
SOURCE: J. Bacteriol. (1993), 175(19), 6082-8
CODEN: JOBAAY; ISSN: 0021-9193
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Radiolabeled penicillin G was used to examine penicillin-binding proteins (PBPs) from Erwinia amylovora (OT1). This procedure identified seven PBPs with mol. masses ranging from 22 to 83 kDa. E. amylovora PBPs were compared with those from Escherichia coli (JM101) and from two spherical, avirulent TnphoA mutants derived from OT1. Radiolabeled penicillin G bound to only six proteins from the spherical mutants which lacked a

69-kDa PBP. The spherical mutants could be complemented by the cloned E. coli pbpA-**rodA** operon, which restored both cell shape and virulence to apple seedlings. This suggested that the E. amylovora 69-kDa PBP is probably the functional equiv. of the E. coli PBP2 protein. Southern blot anal. using the E. coli **rodA** and pbpA genes as radiolabeled probes showed that TnphoA had inserted into the E. amylovora equiv. of the E. coli **rodA**-pbpA operon. Southern blots to chromosomal **DNAs** of the two spherical mutants, using the cloned hrp and dsp genes from E. amylovora as radiolabeled probes, confirmed that the TnphoA factors. Both of the spherical TnphoA mutants synthesized amts. of extracellular polysaccharide equiv. to those synthesized by the wild-type strain (OT1), were resistant to lysis in distd. water and to lysozyme, and elicited the hypersensitive response on nonhost plants. These results indicate a possible role for cell shape in the virulence of this plant pathogen.

L4 ANSWER 11 OF 17 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1993:206613 HCAPLUS
DOCUMENT NUMBER: 118:206613
TITLE: Identification of Aspergillus brlA response elements (BREs) by genetic selection in yeast
AUTHOR(S): Chang, Yun C.; Timberlake, William E.
CORPORATE SOURCE: Dep. Genet., Univ. Georgia, Athens, GA, 30602-7223, USA
SOURCE: Genetics (1993), 133(1), 29-38
CODEN: GENTAE; ISSN: 0016-6731
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The brlA gene of Aspergillus nidulans plays a central role in controlling conidiophore development. To test the hypothesis that brlA encodes a transcriptional regulator and to identify sites of interaction for the BrlA polypeptide, gene brlA was expressed in Saccharomyces cerevisiae strains contg. Aspergillus **DNA** sequences inserted upstream of a minimal yeast promoter fused to the Escherichia coli lacZ gene. Initially, a **DNA** fragment from the promoter region of the developmentally regulated **rodA** gene was tested and shown to mediate brlA-dependent transcriptional activation. Two addnl. **DNA** fragments were selected from an Aspergillus genomic library by their ability to respond to brlA in yeast. These fragments contained multiple copies of a sequence motif present in the **rodA** fragment, which is proposed to be sites for BrlA interaction and designated brlA response elements (BREs). **DNA** fragments contg. BREs upstream of a minimal Aspergillus promoter were capable of conferring developmental regulation in Aspergillus. Deletion of BREs from the upstream region of **rodA** greatly decreased its developmental induction. Multiple copies of a synthetic oligonucleotide with the consensus sequence identified among the BREs mediated brlA-dependent transcriptional activation in yeast. The results show that a primary activity of brlA is transcriptional activation and tentatively identify sites of interaction for the BrlA polypeptide.

L4 ANSWER 12 OF 17 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1993:53505 HCAPLUS
DOCUMENT NUMBER: 118:53505
TITLE: Developmental and light regulation of eas, the structural gene for the rodlet protein of Neurospora
AUTHOR(S): Lauter, Frank Roman; Russo, Vincenzo E. A.; Yanofsky, Charles
CORPORATE SOURCE: Dep. Biol. Sci., Stanford Univ., Stanford, CA, 94305, USA
SOURCE: Genes Dev. (1992), 6(12a), 2373-81
CODEN: GEDEEP; ISSN: 0890-9369
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The surface of many fungal spores is covered by a hydrophobic sheath termed the rodlet layer. The rodlet protein of Neurospora crassa is encoded by a cloned gene designated bli-7. Gene bli-7 is identical to the

known gene eas (easily wettable). Using eas **DNA** as a probe the authors show that eas mRNA is abundant in illuminated mycelia and conidiophores but is not detectable or is barely detectable in dark-grown mycelia, mature macroconidia, microconidia, and ascospores. Mutations in the genes acon-2, acon-3, and fl block early conidiophore development; of these, only fl prevents normal eas transcription. The EAS protein is homologous to the rodlet protein (**RodA**) of Aspergillus nidulans, and the hydrophobins of Schizophyllum commune. Gene eas is the first cloned conidiation (con) gene of N. crassa that is assocd. with a phenotypic alteration.

L4 ANSWER 13 OF 17 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1992:100395 HCAPLUS
DOCUMENT NUMBER: 116:100395
TITLE: Rodletless, a new Aspergillus development mutant induced by directed gene inactivation
AUTHOR(S): Stringer, Mary A.; Dean, Ralph A.; Sewall, Tommy C.; Timberlake, William E.
CORPORATE SOURCE: Dep. Genet., Univ. Georgia, Athens, GA, 30602, USA
SOURCE: Genes Dev. (1991), 5(7), 1161-71
CODEN: GEDEEP; ISSN: 0890-9369
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The Aspergillus nidulans CAN41 transcription unit is activated by the brlA regulatory gene early during development of the asexual reproductive app., the conidiophore. Disruption of CAN41 results in a novel mutant phenotype in which conidiophore cells and spores lack an external wall layer, the rodlet layer, making them less hydrophobic than in the wild type and leading to inefficient spore dispersal. The rodletless mutation defines a new locus on chromosome III, rodA. rodA Encodes a small, moderately hydrophobic polypeptide contg. 8 cysteines arranged in a pattern similar to that obsd. in 3 hydrophobic cell wall proteins from the Holobasidiomycete Schizophyllum commune. It is proposed that the Aspergillus and Schizophyllum 8-cysteine polypeptides define a class of secreted, hydrophobic, fungal cell wall proteins that are important in the formation and function of aerial structures such as conidiophores and mushrooms.

L4 ANSWER 14 OF 17 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1990:566237 HCAPLUS
DOCUMENT NUMBER: 113:166237
TITLE: Revised nucleotide sequence of the sporulation gene spoVE from Bacillus subtilis
AUTHOR(S): Sato, Tsutomu; Theeragool, Gunjana; Yamamoto, Tatsuo; Okamoto, Masaji; Kobayashi, Yasuo
CORPORATE SOURCE: Fac. Agric., Tokyo Univ. Agric. Technol., Fuchu, 183, Japan
SOURCE: Nucleic Acids Res. (1990), 18(13), 4021
CODEN: NARHAD; ISSN: 0305-1048
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The **nucleotide** sequence of the spoVE gene has been detd. previously by U. D. Bugaichuk and P. J. Piggot (1986), and they reported that the spoVE gene consisted of 293 amino acid residues. However, the current study found that 1 **nucleotide** (thymidine) was missing in the **nucleotide** sequence. The addn. of thymidine gave rise to a polypeptide of 40,131 Da (366 aa). Its initiation codon (TTG) is preceded by an SD sequence having DELTA.G of -17.8 kcal/mol. The amino acid sequence of spoVE gene product is highly homologous with that of the newly identified Escherichia coli FtsW and **RodA proteins** functioning in cell division and cell elongation. It is suggested that the SpoVE protein plays an essential role not only during sporulation, but also during vegetative growth.

L4 ANSWER 15 OF 17 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1989:609808 HCAPLUS
DOCUMENT NUMBER: 111:209808

TITLE: **Nucleotide** sequence of the **rodA** gene, responsible for the rod shape of Escherichia coli: **rodA** and the pbpA gene, encoding penicillin-binding protein 2, constitute the **rodA** operon
AUTHOR(S): Matsuzawa, Hiroshi; Asoh, Sadamitsu; Kunai, Kenji; Muraiso, Kanae; Takasuga, Akiko; Ohta, Takahisa
CORPORATE SOURCE: Dep. Agric. Chem., Univ. Tokyo, Tokyo, 113, Japan
SOURCE: J. Bacteriol. (1989), 171(1), 558-60
CODEN: JOBAAY; ISSN: 0021-9193
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The **rodA** gene, which is responsible for the rod shape of E. coli, was located 5 **nucleotides** downstream of another rod-shape-detg. gene, pbpA, encoding penicillin-binding protein 2. The coding region of the **RodA protein** was 1,110 base pairs in length. Two plasmids, carrying a **rodA**-lacZ gene fusion with and without the pbpA promoter upstream of the gene fusion, were constructed. On the basis of the difference between the expression levels of the .beta.-galactosidase activity dependent on and independent of the pbpA promoter, it was concluded that the pbpA and **rodA** genes constitute a single transcriptional unit called the **rodA** operon.

L4 ANSWER 16 OF 17 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1983:518939 HCAPLUS
DOCUMENT NUMBER: 99:118939
TITLE: Identification of the rodA gene product of Escherichia coli
AUTHOR(S): Stoker, Neil G.; Pratt, Julie M.; Spratt, Brian G.
CORPORATE SOURCE: Dep. Genet., Univ. Leicester, Leicester, LE1 7RH, UK
SOURCE: J. Bacteriol. (1983), 155(2), 854-9
CODEN: JOBAAY; ISSN: 0021-9193
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Plasmids that carry the E. coli cell shape gene **rodA** directed the synthesis of a cytoplasmic membrane protein [mol. wt. 31,000 (31K)] in minicells, maxicells, and an in vitro-coupled transcription-translation system. The 31K protein was identified as the **rodA** gene product because it was not synthesized from vector plasmids or from a plasmid in which the **rodA** gene was inactivated by insertion of transposon Tn1000. Furthermore, a purified 1.6-kilobase KpnI-BamHI **DNA** fragment that contained the intact **rodA** gene directed the synthesis of only the 31K protein in an in vitro system. The apparent mol. wt. of the protein was identical whether synthesized in vivo or in vitro, indicating that the **rodA** gene product is not made as a preprotein. The direction of transcription of **rodA** was from the KpnI site towards the BamHI site. The 31K protein was unusual in that it could only be detected when cell membranes were solubilized at low temp. (e.g., 37.degree.) before SDS-polyacrylamide gel electrophoresis. Apparently, the **rodA** gene product aggregates after being boiled in SDS and fails to enter a polyacrylamide gel.

L4 ANSWER 17 OF 17 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1983:174138 HCAPLUS
DOCUMENT NUMBER: 98:174138
TITLE: Molecular cloning and characterization of the genes (pbpA and rodA) responsible for the rod shape of Escherichia coli K-12: analysis of gene expression with transposon Tn5 mutagenesis and protein synthesis directed by constructed plasmids
AUTHOR(S): Asoh, Sadamitsu; Matsuzawa, Hiroshi; Matsuhashi, Michio; Ohta, Takahisa
CORPORATE SOURCE: Inst. Appl. Microbiol., Univ. Tokyo, Tokyo, 113, Japan
SOURCE: J. Bacteriol. (1983), 154(1), 10-16
CODEN: JOBAAY; ISSN: 0021-9193
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Two cell shape-detg. genes of E. coli K-12, pbpA, the structural gene for penicillin-binding protein 2, and **rodA**, the protein of which is unknown, were subcloned into plasmid vectors from the transducing phage .lambda.MAd lip24, which carries the lip-leuS region of the E. coli chromosome. Plasmids with restriction enzyme-created deletions of transposon Tn5 insertions were isolated, and studies of genetic complementation of these plasmids with chromosomal mutations were carried out. Thus, a phys. and genetic map of the **rodA**-pbpA region was established. The genes **rodA** and pbpA lie side by side within a 4.4-kilobase-pair region. The size of the **rodA** gene is 0.86-1.6 kilobase pairs; such **DNA** could encode a protein of mol. wt. 32,000-59,000. Since Tn5 mutagenesis of the **rodA** gene did not affect the expression of the pbpA gene and vice versa, the genes **rodA** and pbA seem to have independent promoters. Examn. of the proteins encoded by the constructed plasmids in maxicells revealed that the plasmid carrying the pbpA gene encoded penicillin-binding protein 2, and amplification of the protein occurred. The product of the **rodA** gene was not identified.